**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

| | | | |
|---|---|---|---|
| In re application of: | Holtzman, Douglas A. | | |
| Application No.: | 09/782,980 | Group No.: | 1652 |
| Filed: | February 13, 2001 | Examiner: | Maryam Monshipouri, Ph.D. |
| For: | NOVEL ITALY, LOR-2, STRIFE, TRASH, BDSF, LRSG, AND STMST PROTEIN AND NUCLEIC ACID MOLECULES AND USES THEREFOR | | |

Commissioner for Patents
Washington, DC 20231

## RESPONSE TO RESTRICTION REQUIREMENT

Dear Madam:

### REMARKS

In response to the Restriction Requirement dated June 12, 2003 (Paper No. 11), Applicants hereby elect Group 9b, drawn to isolated DNA sequences encoding human STMST-2 polypeptides, host cells, kits comprising said sequences, and methods of expressing said sequences (claims 1-7, 12, 18, and 53-54), with traverse. This election is made without prejudice to Applicant's right to pursue the non-elected subject matter in other applications in the event a generic claim is not found allowable.

Applicants respectfully traverse the present restriction and reserve the right to petition therefrom under 37 C.F.R. § 1.144 and for the reasons set forth below.

---

**CERTIFICATION UNDER 37 C.F.R. SECTIONS 1.8(a) and 1.10***

I hereby certify that, on the date shown below, this correspondence is being:

**MAILING**

☑ deposited with the United States Postal Service in an envelope addressed to the Commissioner for Patents, Washington, D.C. 20231.
**37 C.F.R. SECTION 1.8(a)**

☑ with sufficient postage as first class mail.

☐ as "Express Mail Post Office to Address" Mailing Label No.
**37 C.F.R. SECTION 1.10***

**TRANSMISSION**

☐ transmitted by facsimile to the Patent and Trademark Office.

Signature Mary MacKinnon

Date: July 14, 2003

Mary MacKinnon
*(type or print name of person certifying)*



#12 Dig 7/14/03

**Elected as Separate Species of a Common Genus**

Applicants submit that the separate nucleic acid sequences encoding SEQ ID NOs:71 and 74 (STMST-1 and STMST-2, respectively) should be examined together, as species of a common genus. As seen in the enclosed protein sequence alignment (**Exhibit A**), the sequences of SEQ ID NOs:71 and 74 (and the nucleic acid sequences encoding them) are related in that SEQ ID NO:74 (STMST-2), which is a 609 residue protein, comprises the majority portion of SEQ ID NO:71 (STMST-1), which is a 297 residue protein. Both protein sequences share the first 262 residues, which constitute over 88% of the entire length of the STMST-1 protein. The nucleic acid sequence encoding the protein sequences are even more similar, as evidenced by the enclosed alignment of the open reading frame encoding STMST-1 and a truncated version of the open reading frame encoding STMST-2 (**Exhibit B**, showing 93% sequence identity over the length of the STMST-1 open reading frame).

The inclusion of both nucleic acids which encode SEQ ID NOs:71 and 74 in the current election does not pose a serious examination burden on the Examiner. In fact, it would require virtually the same search and examination, since searching and examining nucleic acids that encode SEQ ID NO:74 includes by necessity a search and examination of the nucleic acids that encode SEQ ID NO:71 (SEQ ID NO:71 shares residues 1-262 of SEQ ID NO:74).

This paper is being filed timely, as it is believed that no extensions of time are required. In the event any extensions of time are deemed necessary, the undersigned hereby authorizes the requisite fees to be charged to Deposit Account No. 501668.

Entry of the remarks made herein is respectfully requested.

Respectfully submitted,

July 14, 2003

MILLENNIUM PHARMACEUTICALS, INC.

By _____

Paul J. Paglierani
Registration No. 52,498
75 Sidney Street
Cambridge, MA 02139
Telephone - 617-761-6865
Facsimile - 617-551-8820

```
>STMST1                                                    --- --- ---
>STMST2                                                    609 aa
scoring matrix: BLOSUM50, gap penalties: -12/-2
46.8% identity;          Global alignment score: 1198

                10        20        30        40        50        60
STMST2 MSDERRLPGSAVGWLVCGGLSLLANAWGILSVGAKQKKWKPLEFLLCTLAATHMLNVAVP
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
STMST2 MSDERRLPGSAVGWLVCGGLSLLANAWGILSVGAKQKKWKPLEFLLCTLAATHMLNVAVP
                10        20        30        40        50        60

                70        80        90       100       110       120
STMST1 IATYSVVQLRRQRPDFEWNEGLCKVFVSTFYTLTLATCFSVTSLSYHRMWMVCWPVNYRL
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
STMST2 IATYSVVQLRRQRPDFEWNEGLCKVFVSTFYTLTLATCFSVTSLSYHRMWMVCWPVNYRL
                70        80        90       100       110       120

               130       140       150       160       170       180
STMST1 SNAKKQAVHTVMGIWMVSFILSALPAVGWHDTSERFYTHGCRFIVAEIGLGFGVCFLLLV
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
STMST2 SNAKKQAVHTVMGIWMVSFILSALPAVGWHDTSERFYTHGCRFIVAEIGLGFGVCFLLLV
               130       140       150       160       170       180

               190       200       210       220       230       240
STMST1 GGSVAMGVICTAIALFQTLAVQVGRQADHRAFTVPTIVVEDAQGKRRSSIDGSEPAKTSL
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
STMST2 GGSVAMGVICTAIALFQTLAVQVGRQADHRAFTVPTIVVEDAQGKRRSSIDGSEPAKTSL
               190       200       210       220       230       240

                    250       260
STMST1 QTTGLVTTIVFIYDCLMGFPVL---------D-STP----------------IP------
       :::::::::::::::::::::::         : :.:                .:
STMST2 QTTGLVTTIVFIYDCLMGFPVLVVSFSSLRADASAPWMALCVLWCSVAQALLLPVFLWAC
                    250       260       270       280       290       300

                                                       270
STMST1 ------------------------------------------ERS----------------
                                                    :::
STMST2 DRYRADLKAVREKCMALMANDEESDDETSLEGGISPDLVLERSLDYGYGGDFVALDRMAK
                    310       320       330       340       350       360

                                                                  280
STMST1 ----AVRQG-----------ED-------------------------------------WG----
           :.. :           ::                                     ::
STMST2 YEISALEGGLPQLYPLRPLQEDKMQYLQVPPTRRFSHDDADVWAAVPLPAFLPRWGSGED
                    370       380       390       400       410       420

STMST1 ---------------------------------------------------------KDQPE
                                                                .:.: .
STMST2 LAALAHLVLPAGPERRRASLLAFAEDAPPSRARRRSAESLLSLRTSALDSGPRGARDSPP
                    430       440       450       460       470       480

STMST1 G------------------------FH-------------------------------
       :                        :.
STMST2 GSPRRRPGPGPRSASASLLPDAFALTAFECEPQALRRPPGPFPAAPAAPDGADPGEAPTP
                    490       500       510       520       530       540

           290
STMST1 PSSRQ-----------------------------------------------------
```

STMST1 --DCL---P
STMST2 HSDSLGSAS

Received from < 617 551 8820 > at 7/14/03 3:52:43 PM [Eastern Daylight Time]

>stmst1 891 nt
>stmst2 (truncated)
scoring matrix: DNA, gap penalties: -16/-4
93.0% identity; Global alignment score: 3863

```
                10        20        30        40        50        60
/tmp/s ATGAGTGATGAGCGGCGGCTGCCTGGCAGTGCAGTGGGCTGGCTGGTATGTGGGGGCCTC
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
stmst2 ATGAGTGATGAGCGGCGGCTGCCTGGCAGTGCAGTGGGCTGGCTGGTATGTGGGGGCCTC
                10        20        30        40        50        60

                70        80        90       100       110       120
/tmp/s TCCCTGCTGGCCAATGCCTGGGGCATCCTCAGCGTTGGCGCCAAGCAGAAGAAGTGGAAG
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
stmst2 TCCCTGCTGGCCAATGCCTGGGGCATCCTCAGCGTTGGCGCCAAGCAGAAGAAGTGGAAG
                70        80        90       100       110       120

               130       140       150       160       170       180
/tmp/s CCCTTGGAGTTCCTGCTGTGTACGCTCGCGGCCACCCACATGCTAAATGTGGCCGTGCCC
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
stmst2 CCCTTGGAGTTCCTGCTGTGTACGCTCGCGGCCACCCACATGCTAAATGTGGCCGTGCCC
               130       140       150       160       170       180

               190       200       210       220       230       240
/tmp/s ATCGCCACCTACTCCGTGGTGCAGCTGCGGCGGCAGCGCCCCGACTTCGAGTGGAATGAG
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
stmst2 ATCGCCACCTACTCCGTGGTGCAGCTGCGGCGGCAGCGCCCCGACTTCGAGTGGAATGAG
               190       200       210       220       230       240

               250       260       270       280       290       300
/tmp/s GGTCTCTGCAAGGTCTTCGTGTCCACCTTCTACACCCTCACCCTGGCCACCTGTTTCTCT
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
stmst2 GGTCTCTGCAAGGTCTTCGTGTCCACCTTCTACACCCTCACCCTGGCCACCTGTTTCTCT
               250       260       270       280       290       300

               310       320       330       340       350       360
/tmp/s GTCACCTCCCTCTCCTACCACCGCATGTGGATGGTCTGCTGGCCTGTCAACTACCGGCTG
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
stmst2 GTCACCTCCCTCTCCTACCACCGCATGTGGATGGTCTGCTGGCCTGTCAACTACCGGCTG
               310       320       330       340       350       360

               370       380       390       400       410       420
/tmp/s AGCAATGCCAAGAAGCAGGCGGTGCACACAGTCATGGGTATCTGGATGGTGTCCTTCATC
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
stmst2 AGCAATGCCAAGAAGCAGGCGGTGCACACAGTCATGGGTATCTGGATGGTGTCCTTCATC
               370       380       390       400       410       420

               430       440       450       460       470       480
/tmp/s CTGTCGGCCCTGCCTGCCGTTGGCTGGCACGACACCAGCGAGCGCTTCTACACCCATGGC
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
stmst2 CTGTCGGCCCTGCCTGCCGTTGGCTGGCACGACACCAGCGAGCGCTTCTACACCCATGGC
               430       440       450       460       470       480

               490       500       510       520       530       540
/tmp/s TGCCGCTTCATCGTGGCTGAGATCGGCCTGGGCTTTGGCGTCTGCTTCCTGCTGCTGGTG
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
stmst2 TGCCGCTTCATCGTGGCTGAGATCGGCCTGGGCTTTGGCGTCTGCTTCCTGCTGCTGGTG
               490       500       510       520       530       540

               550       560       570       580       590       600
/tmp/s GGCGGCAGCGTGGCCATGGGCGTGATCTGCACAGCCATCGCCCTCTTCCAGACGCTGGCC
```

```
                610        620        630        640        650        660
/tmp/s GTGCAGGTGGGGCGCCAGGCCGACCACCGCGCCTTCACCGTGCCCACCATCGTGGTGGAG
       :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
stmst2 GTGCAGGTGGGGCGCCAGGCCGACCACCGCGCCTTCACCGTGCCCACCATCGTGGTGGAG
                610        620        630        640        650        660

                670        680        690        700        710        720
/tmp/s GACGCGCAGGGCAAGCGGCGCTCCTCCATCGATGGCTCGGAGCCCGCCAAAACCTCTCTG
       :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
stmst2 GACGCGCAGGGCAAGCGGCGCTCCTCCATCGATGGCTCGGAGCCCGCCAAAACCTCTCTG
                670        680        690        700        710        720

                730        740        750        760        770        780
/tmp/s CAGACCACGGGCCTCGTGACCACCATAGTCTTCATCTACGACTGCCTCATGGGCTTCCCT
       :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
stmst2 CAGACCACGGGCCTCGTGACCACCATAGTCTTCATCTACGACTGCCTCATGGGCTTCCCT
                730        740        750        760        770        780

                790        800        810        820        830
/tmp/s GTGCTGGACTCTACGCCCATCCCCGAAAGGTCTGCAGTGAGACAGGG-AGAGGACTGG--
       :::::::     :    :: :  :       :::: :   :::     :: :  ::::
stmst2 GTGCTGGTGGTGAGCTTCAGCAGC-------CTGCGGGCCGACGCCTCAGCGCCCTGGAT
                790        800                810        820        830

       840        850        860            870        880        890
/tmp/s GGCAAAGACCAGCCTGAGGGGTTTCAT---CCAAGCAGCAGGCAAGACTGCCTTCC-C
       ::::     :   ::: :: : : : :   ::: ::           : :::  :::: :
stmst2 GGCACTCTGCGTGCTGTGGTGCTCCGTGGCCCAGGCCCTGCTGCTGCCTGTGTTCCTC
            840        850        860        870        880        890
```

Office, Washington, DC 20231. DO NOT SEND FEES OR COMPLETED FORMS TO THIS ADDRESS. SEND TO:

Patents,
Washington, DC 20231.

**Practitioner's Docket No. MPI00-544OMNIM** ***PATENT***



## Certificate of Transmission under 37 CFR 1.8

I hereby certify that this correspondence is being facsimile transmitted to the United States Patent and Trademark Office

On July 14, 2003.

Mary MacKinnon
Signature

Mary MacKinnon
Typed or printed name of person signing Certificate

Note: Each paper must have its own certificate of transmission, or this certificate must identify each submitted paper.

**Submitted herewith:**

| | |
|---|---|
| Response to Restriction Requirement | (2 pages) |
| Exhibit A | (2 pages) |
| Exhibit B | (2 pages) |
| Total | (7 pages-including fax cover sheet) |